IN THE CLAIMS

Please amend the claims as follows:

1-29. (Canceled)

30. (Previously presented) A process for the production of a *Haemophilus influenzae*-specific lipooligosaccharide (LOS) which comprises the steps of:

(a) growing in a culture medium gram-negative bacteria comprising (i) a core lipid structure containing a terminal heptose and (ii) a DNA sequence encoding an Undecaprenyl-phosphate N-acetyl glucosaminyl phosphate transferase (*rfe*), and (iii) an isolated DNA sequence encoding a lipooligosaccharide-synthesis gene G polypeptide (LsgG) from *Haemophilus influenzae*, wherein the DNA sequence encoding *rfe* is regulated by LsgG such that a *H. influenzae*-specific LOS is synthesized by the addition of an acceptor molecule to the terminal heptose molecule; and

(b) recovering the *H. influenzae*-specific LOS from the culture medium.

31. (Previously presented) The process of claim 30, wherein the bacteria are *Escherichia coli.*

32. (Previously presented) The process of claim 31, wherein the bacteria are *Escherichia coli* K-12 strain JM 109.

33. (Previously presented) The process of claim 30, wherein the bacteria are *Salmonella minnesota.*

34. (Previously presented) The process of claim 30, wherein the acceptor molecule is N-acetylglucosamine.

35. (Previously presented) The process of claim 30, wherein the DNA sequence encoding *rfe* is from *Haemophilus influenzae.*

36. (Previously presented) The process of claim 30, wherein the DNA sequence encoding a *rfe* is part of the gram-negative bacterial genome.

37. (Previously presented) The process of claim 30, wherein the isolated DNA sequence encoding the LsgG is comprised in a vector.

38. (Previously presented) The process of claim 30, wherein the bacteria further comprise a glycosyltransferase.

39. (Currently amended) A process for the production of a complex carbohydrate comprising the steps of:

(a) growing in a culture medium gram-negative bacteria comprising (i) a core lipid structure containing a terminal heptose and (ii) a DNA sequence encoding an Undecaprenyl-phosphate N-acetyl glucosaminyl phosphate transferase (*rfe*), and (iii) an isolated DNA sequence encoding a ~~liposaccharide-synthesis~~ lipooligosaccharide-synthesis gene G polypeptide (LsgG) from *Haemophilus influenzae*, wherein the DNA sequence encoding *rfe* is regulated by LsgG such that a complex carbohydrate is synthesized by the addition of an acceptor molecule to the heptose molecule; and

(b) recovering the complex carbohydrate from the culture medium.

40. (Previously presented) The process of claim 39, wherein the bacteria are *Escherichia coli.*

41. (Previously presented) The process of claim 40, wherein the bacteria are *Escherichia coli* K-12 strain JM 109.

42. (Previously presented) The process of claim 39, wherein the bacteria are *Salmonella minnesota.*

43. (Previously presented) The process of claim 39, wherein the acceptor molecule is N-acetylglucosamine.

44. (Previously presented) The process of claim 39, wherein the DNA sequence encoding *rfe* is from *Haemophilus influenzae*.

45. (Previously presented) The process of claim 39, wherein the DNA sequence encoding a *rfe* is part of the gram-negative bacterial genome.

46. (Previously presented) The process of claim 39, wherein the isolated DNA sequence encoding LsgG is contained in a vector.

47. (Previously presented) The process of claim 39, wherein the bacteria further comprise a glycosyltransferase.

48. (Currently amended) A method ~~of~~ comprising modifying a terminal heptose of a lipopolysaccharide (LPS) or lipooligosaccharide (LOS) core structure of a gram-negative bacterial species, wherein the gram-negative bacterial species comprises ~~comprising~~ a polynucleotide encoding an Undecaprenyl-phosphate N-acetyl glucosaminyl phosphate transferase (*rfe*) and an isolated DNA sequence encoding a lipooligosaccharide-synthesis gene G polypeptide (LsgG) from *Haemophilus influenzae*, wherein the polynucleotide encoding *rfe* is regulated by lipooligosaccharide-synthesis gene G polypeptide (LsgG) from *Haemophilus influenzae* such that an N-acetyl glucosamine is added onto the terminal heptose so as to modify the terminal heptose, wherein the gram-negative bacterial species is *Salmonella minnesota*.

49. (Previously presented) The method of claim 48 wherein the bacteria are *Escherichia coli*.

50. (Previously presented) The method of claim 49, wherein the bacteria are *Escherichia coli* K-12 strain JM 109.

51. (Canceled)

52. (Previously presented) The method of claim 48, wherein the polynucleotide encoding *rfe* is from *Haemophilus influenzae*.

53. (Previously presented) The method of claim 48, wherein the polynucleotide encoding *rfe* is part of the gram-negative bacterial genome.

54. (Previously presented) The method of claim 48, wherein a polynucleotide encoding the LsgG is comprised in a vector.

55. (Previously presented) The method of claim 48, wherein the bacteria further comprise a glycosyltransferase.

56. (New) The process of claim 38, wherein the glycosyltransferase is a *Haemophilus influenzae* glycosyltransferase.

57. (New) The process of claim 47, wherein the glycosyltransferase is a *Haemophilus influenzae* glycosyltransferase.

58. (New) The method of claim 55, wherein the glycosyltransferase is a *Haemophilus influenzae* glycosyltransferase.